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TECH CENTER 1600/2030



1600

RAW SEQUENCE LISTING

DATE: 08/28/2003

PATENT APPLICATION: US/09/785,548A

TIME: 11:26:48

Input Set : A:\ST0005_SeqListing.txt

Output Set: N:\CRF4\08282003\I785548A.raw

3 <110> APPLICANT: Brice, Alexis
 4 Koutnikova, Hana
 5 Fournier, Alain
 6 Pradier, Laurent
 7 Prades, Catherine
 8 Arnould-Reguigne, Isabelle
 9 Rosier-Montus, Marie-Francoise
 10 Corti, Olga
 12 <120> TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF
 PARKIN
 14 <130> FILE REFERENCE: ST00005
 16 <140> CURRENT APPLICATION NUMBER: 09/785,548A
 17 <141> CURRENT FILING DATE: 2001-02-20
 19 <160> NUMBER OF SEQ ID NOS: 50
 21 <170> SOFTWARE: PatentIn Version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1313
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 29 cag aat ctc cca tcc agt ccg gca ccc agt acc ata ttc tct gga ggt 48
 30 Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly
 31 1 5 10 15
 33 ttt aga cac gga agt tta att agc att gac agc acc tgt aca gag atg 96
 34 Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met
 35 20 25 30
 37 ggc aat ttt gac aat gct aat gtc act gga gaa ata gaa ttt gcc att 144
 38 Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile
 39 35 40 45
 41 cat tat tgc ttc aaa acc cat tct tta gaa ata tgc atc aag gcc tgt 192
 42 His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
 43 50 55 60
 45 aag aac ctt gcc tat gga gaa gaa aag aag aaa aag tgc aat ccg tat 240
 46 Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
 47 65 70 75 80
 49 gtg aag acc tac ctg ttg ccc gac aga tcc tcc cag gga aag cgc aag 288
 50 Val Lys Thr Tyr Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
 51 85 90 95
 53 act gga gtc caa agg aac acc gtg gac ccg acc ttt cag gag acc ttg 336
 54 Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
 55 100 105 110
 57 aag tat cag gtg gcc cct gcc cag ctg gtg acc cgg cag ctg cag gtc 384
 58 Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
 59 115 120 125

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61 tcg gtg tgg cat ctg ggc acg ctg gcc cgg aga gtg ttt ctt gga gaa 432
62 Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
63 130 135 140
65 gtg atc att tct ctg gcc acg tgg gac ttt gaa gac agc aca aca cag 480
66 Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
67 145 150 155 160
69 tcc ttc cgc tgg cat ccg ctc cgg gcc aag gcg gag aaa tac gaa gac 528
70 Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
71 165 170 175
73 agc gtt cct cag agt aat gga gag ctc aca gtc cgg gct aag ctg gtt 576
74 Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
75 180 185 190
77 ctc cct tca cgg ccc aga aaa ctc caa gag gct caa gaa ggg aca gat 624
78 Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
79 195 200 205
81 cag cca tca ctt cat ggt caa ctt tgt ttg gta gtg cta gga gcc aag 672
82 Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
83 210 215 220
85 aat tta cct gtg cgg cca gat ggc acc ttg aac tca ttt gtt aag ggc 720
86 Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
87 225 230 235 240
89 tgt ctc act ctg cca gac caa caa aaa ctg aga ctg aag tcg cca gtc 768
90 Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
91 245 250 255
93 ctg agg aag cag gct tgc ccc cag tgg aaa cac tca ttt gtc ttc agt 816
94 Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
95 260 265 270
97 ggc gta acc cca gct cag ctg agg cag tcg agc ttg gag tta act gtc 864
98 Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
99 275 280 285
101 tgg gat cag gcc ctc ttt gga atg aat gac cgc ttg ctt gga gga acc 912
102 Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
103 290 295 300
105 aga ctt ggt tca aag gga gac aca gct gtt ggc ggg gat gca tgc tca 960
106 Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
107 305 310 315 320
109 cta tcg aag ctc cag tgg cag aaa gtc ctt tcc agc ccc aat cta tgg 1008
110 Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
111 325 330 335
113 aca gac atg act ctt gtc ctg cac tgacatgaag gcctcaaggt tccagggttc 1062
114 Thr Asp Met Thr Leu Val Leu His
115 340
117 agcaggcggtg aggcactgtg cgtctgcaga ggggctacga accagggtgca ggggtcccagc 1122
119 tggagacccc tttgaccttg agcagtcctcc atctgcggcc ctgtcccatg gcttaaccgc 1182
121 ctattggtat ctgtgtatat ttacgttaaa cacaattatg ttacctaagc ctctggtggg 1242
123 ttatctcctc tttgagatgt agaaaatggc cagattttaa taaacgttgt taccocatgaa 1302
125 aaaaaaaaaa a 1313
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 344

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130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
134 Gln Asn Leu Pro Ser Ser Pro Ala Pro Ser Thr Ile Phe Ser Gly Gly
135 1 5 10 15
137 Phe Arg His Gly Ser Leu Ile Ser Ile Asp Ser Thr Cys Thr Glu Met
138 20 25 30
140 Gly Asn Phe Asp Asn Ala Asn Val Thr Gly Glu Ile Glu Phe Ala Ile
141 35 40 45
143 His Tyr Cys Phe Lys Thr His Ser Leu Glu Ile Cys Ile Lys Ala Cys
144 50 55 60
146 Lys Asn Leu Ala Tyr Gly Glu Glu Lys Lys Lys Lys Cys Asn Pro Tyr
147 65 70 75 80
149 Val Lys Thr Tyr Leu Leu Pro Asp Arg Ser Ser Gln Gly Lys Arg Lys
150 85 90 95
152 Thr Gly Val Gln Arg Asn Thr Val Asp Pro Thr Phe Gln Glu Thr Leu
153 100 105 110
155 Lys Tyr Gln Val Ala Pro Ala Gln Leu Val Thr Arg Gln Leu Gln Val
156 115 120 125
158 Ser Val Trp His Leu Gly Thr Leu Ala Arg Arg Val Phe Leu Gly Glu
159 130 135 140
161 Val Ile Ile Ser Leu Ala Thr Trp Asp Phe Glu Asp Ser Thr Thr Gln
162 145 150 155 160
164 Ser Phe Arg Trp His Pro Leu Arg Ala Lys Ala Glu Lys Tyr Glu Asp
165 165 170 175
167 Ser Val Pro Gln Ser Asn Gly Glu Leu Thr Val Arg Ala Lys Leu Val
168 180 185 190
170 Leu Pro Ser Arg Pro Arg Lys Leu Gln Glu Ala Gln Glu Gly Thr Asp
171 195 200 205
173 Gln Pro Ser Leu His Gly Gln Leu Cys Leu Val Val Leu Gly Ala Lys
174 210 215 220
176 Asn Leu Pro Val Arg Pro Asp Gly Thr Leu Asn Ser Phe Val Lys Gly
177 225 230 235 240
179 Cys Leu Thr Leu Pro Asp Gln Gln Lys Leu Arg Leu Lys Ser Pro Val
180 245 250 255
182 Leu Arg Lys Gln Ala Cys Pro Gln Trp Lys His Ser Phe Val Phe Ser
183 260 265 270
185 Gly Val Thr Pro Ala Gln Leu Arg Gln Ser Ser Leu Glu Leu Thr Val
186 275 280 285
188 Trp Asp Gln Ala Leu Phe Gly Met Asn Asp Arg Leu Leu Gly Gly Thr
189 290 295 300
191 Arg Leu Gly Ser Lys Gly Asp Thr Ala Val Gly Gly Asp Ala Cys Ser
192 305 310 315 320
194 Leu Ser Lys Leu Gln Trp Gln Lys Val Leu Ser Ser Pro Asn Leu Trp
195 325 330 335
197 Thr Asp Met Thr Leu Val Leu His
198 340
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 471

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204 <212> TYPE: DNA
205 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (1)..(471)
211 <400> SEQUENCE: 3
212 gga agt cca gca ggt aga tca atc tac aac agc ttt tat gtg tat tgc 48
213 Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
214 1 5 10 15
216 aaa ggc ccc tgt caa aga gtg cag ccg gga aaa ctc agg gta cag tgc 96
217 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
218 20 25 30
220 agc acc tgc agg cag gca acg ctc acc ttg acc cag ggt cca tct tgc 144
221 Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
222 35 40 45
224 tgg gat gat gtt tta att cca aac cgg atg agt ggt gaa tgc caa tcc 192
225 Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
226 50 55 60
228 cca cac tgc cct ggg act agt gca gaa ttt ttc ttt aaa tgt gga gca 240
229 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
230 65 70 75 80
232 cac ccc acc tct gac aag gaa aca tca gta gct ttg cac ctg atc gca 288
233 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
234 85 90 95
236 aca aat agt cgg aac atc act tgc att acg tgc aca gac gtc agg agc 336
237 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
238 100 105 110
240 ccc gtc ctg gtt ttc cag tgc aac tcc cgc cac gtg att tgc tta gac 384
241 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
242 115 120 125
244 tgt ttc cac tta tac tgt gtg aca aga ctc aat gat cgg cag ttt gtt 432
245 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
246 130 135 140
248 cac gac cct caa ctt ggc tac tcc ctg cct tgt gtg tag 471
249 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
250 145 150 155
253 <210> SEQ ID NO: 4
254 <211> LENGTH: 156
255 <212> TYPE: PRT
256 <213> ORGANISM: Homo sapiens
258 <400> SEQUENCE: 4
259 Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn Ser Phe Tyr Val Tyr Cys
260 1 5 10 15
261 Lys Gly Pro Cys Gln Arg Val Gln Pro Gly Lys Leu Arg Val Gln Cys
262 20 25 30
263 Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu Thr Gln Gly Pro Ser Cys
264 35 40 45
265 Trp Asp Asp Val Leu Ile Pro Asn Arg Met Ser Gly Glu Cys Gln Ser
266 50 55 60

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267 Pro His Cys Pro Gly Thr Ser Ala Glu Phe Phe Phe Lys Cys Gly Ala
268 65 70 75 80
269 His Pro Thr Ser Asp Lys Glu Thr Ser Val Ala Leu His Leu Ile Ala
270 85 90 95
271 Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg Ser
272 100 105 110
273 Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu Asp
274 115 120 125
275 Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe Val
276 130 135 140
277 His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val
278 145 150 155
282 <210> SEQ ID NO: 5
283 <211> LENGTH: 27
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial sequence
287 <220> FEATURE:
288 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
290 <400> SEQUENCE: 5
291 ttaagaattc ggaagtccag caggtag 27
294 <210> SEQ ID NO: 6
295 <211> LENGTH: 29
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
302 <400> SEQUENCE: 6
303 attagatcc ctacacacaa ggcagggag 29
306 <210> SEQ ID NO: 7
307 <211> LENGTH: 19
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
314 <400> SEQUENCE: 7
315 gcgttttgaa tcactacag 19
318 <210> SEQ ID NO: 8
319 <211> LENGTH: 17
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of the artificial sequence:Oligonucleotide
326 <400> SEQUENCE: 8
327 ggtctcggtg tggcatc 17
330 <210> SEQ ID NO: 9
331 <211> LENGTH: 18
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial sequence
335 <220> FEATURE:

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VERIFICATION SUMMARY

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